

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 22:34:15 ; Search time 7192 Seconds
(without alignments)
7351.400 Million cell updates/sec

Title: US-10-695-243-3

Sequence: 1 atgcgaataatcgaagaag.....aacagcagccttcataa 1389

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gse1:
9: gb_gse2:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1389	100.0	3404 3 AK030141	AK030141 Mus muscu
2	778.4	56.0	783 7 CK638784	CK638784 UT-M-HO-
3	753.4	54.2	757 6 CB722971	CB722971 UT-M-GH-
4	713.4	51.4	726 6 CB722993	CB722993 UT-M-GH-
5	711.6	51.2	719 7 CO431563	CO431563 UT-M-HX-
6	706.4	50.9	717 7 CK639206	CK639206 UT-M-HO-
7	704.4	50.7	737 7 CN536849	CN536849 UT-M-HO-
8	669.8	48.2	818 7 CN537400	CN537400 UT-M-HO-
9	666	47.9	681 7 CN533939	CN533939 UT-M-HO-
10	621.8	44.8	796 7 CN258978	CN258978 17006001
11	596	42.9	702 7 CF728873	CF728873 UT-M-HO-
12	587.4	42.3	589 6 CA878786	CA878786 K0969D12-
13	557.6	40.1	668 2 BB616889	BB616889 BB616889
14	520.4	37.5	633 9 CG589448	CG589448 OST241683
15	512	36.9	863 1 AJ813286	AJ813286 AJ813286
16	502.4	36.2	504 6 CA878760	CA878760 K0969C10-
17	495.2	35.7	778 4 BG194979	BG194979 RST14037
18	494.4	35.6	480 7 CN455409	CN455409 UT-M-HO-
19	480	34.6	480 7 CF907159	CF907159 A0507A10-
20	449	32.3	739 9 AG437766	AG437766 Mus muscu
21	425	30.6	840 4 BG286536	BG286536 602382535
22	424.6	30.3	487 6 CB726469	CB726469 MGNNTC:C
23	420.6	30.3	765 7 CK774533	CK774533 963302 MA
24	414.2	29.8	591 4 B1848382	B1848382 470812 MA

25	394	28.4	634	4	BM729307	UI-E-E01-
26	391	28.1	460	7	CK344479	K0955A10-
27	372.4	26.8	632	4	BM781108	MLN1_4_E0
28	369.4	26.6	651	5	BK471708	DKF2686B
29	365.4	26.3	678	1	AL710783	DKF2686E
30	361	26.0	614	5	BH218698	603756354
31	357.6	25.7	799	5	BU365777	603784922
32	351.2	25.3	824	9	AY412826	Mus muscu
33	350	25.2	576	6	CD683768	EST288 hu
34	343.4	24.7	583	5	BK472485	DKF2686J
35	341.6	24.6	824	9	AY412824	Homo sapi
36	340.2	24.5	752	7	CK596565	AGENCOURT
37	336.8	24.2	811	9	AY412825	pan trogl
38	329.2	23.7	609	7	CR753261	DKF26493K
39	318.2	22.9	637	5	BU346013	60416885
40	305	22.0	610	5	BK481372	DKF2686M
41	280	20.2	280	2	BF151483	uz15h10.Y
42	276.4	19.9	586	5	BP326282	BP326282
43	275	19.8	790	4	BG386631	602454883
44	274.8	19.8	827	5	BU386802	603581728
45	273.4	19.7	521	7	CN277241	17006001

ALIGNMENTS

RESULT 1
AK030141
LOCUS
DEFINITION
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932703L02 product:ENNO-ALPHA-D-MANNOSIDASE homolog (Rattus norvegicus), full insert sequence.

ACCESSION
AK030141.1 GI:26326122
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
MEDLINE
PUBMED
99279253
10349636

REFERENCES

AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
11042159
REFERENCES
AUTHORS
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
20499374
11042159

TITLE
JOURNAL
MEDLINE
PUBMED
20530913
11078661
REFERENCES
AUTHORS
4
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
JOURNAL
MEDLINE
PUBMED
5
The PANTOM Consortium and the RIKEN Genome Exploration Research

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 18:09:50 ; Search time 10073 Seconds

(without alignments)
6681.653 Million cell updates/sec

Title: US-10-695-243-1

Perfect score: 1389

Sequence: 1 atggcaagatttcgagagaag.....gccagctgcctcttctta 1389

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl1.*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1389	100.0	1389	6	CQ868818 Sequence
2	1387.4	99.9	4386	6	CQ491652 Sequence
3	1387.4	99.9	4386	6	CQ497537 Sequence
4	1387.4	99.9	4596	6	HSMB06986 Sequence
5	1385.8	99.8	1474	9	HSAS77574 Homo sapi
6	1385.8	99.8	4558	9	HSMB05695 Sequence
7	1075	77.4	2388	6	BD159701 Homo sapi
8	1075	77.4	2388	6	AX882397 Sequence
9	1075	77.4	2388	6	AK022900 Homo sapi
10	1065.8	76.7	4645	10	BC067076 Mus muscu
11	1064.2	76.6	1389	6	CQ868820 Sequence
12	929.4	66.9	2552	10	AF023657 Rattus no
13	706.8	50.9	1408	5	CR354351 Gallus ga
14	656.8	47.3	105273	9	AL671884 Human DNA
15	640.8	46.1	2779	5	BC077304 Xenopus la
16	599	43.1	782	9	AY048774 Homo sapi
17	549.2	39.5	1096	9	AY048775 Homo sapi
18	514.2	37.0	193704	10	AL805949 Mouse DNA
19	513.2	36.9	713	6	CQ482870 Sequence

20	509.4	36.7	256771	2	AC115326	AC115326 Rattus no
21	456.8	32.9	2770	10	BC065047	BC065047 Mus muscu
22	408.8	29.4	1083	6	CQ722353	CQ722353 Sequence
23	408.8	29.4	2310	6	AR541894	AR541894 Sequence
24	372	26.8	584	6	CQ503974	CQ503974 Sequence
25	372	26.8	584	6	CQ512775	CQ512775 Sequence
26	356	25.6	1859	9	BC063587	BC063587 Homo sapi
27	284	20.4	348	6	BD148022	BD148022 Homo sapi
28	284	20.4	348	6	AX867960	AX867960 Sequence
29	281.8	20.3	3286	5	BC081681	BC081681 Danio rer
30	277.6	20.0	197552	10	AL606933	AL606933 Mouse DNA
31	277	19.9	449	6	CQ473701	CQ473701 Sequence
32	270.4	19.5	797	11	BV174680	BV174680 segm73513
33	259.6	19.4	181070	2	AC142187	AC142187 Rattus no
34	259.6	19.4	123789	2	AC110674	AC110674 Tetradon
35	256	18.4	1246	5	BX930133	BX930133 Gallus ga
36	255.2	18.4	2341	6	AX714001	AX714001 Sequence
37	255.2	18.4	2341	9	AK055996	AK055996 Homo sapi
38	255.2	18.4	134161	9	AC104336	AC104336 Homo sapi
39	255.2	18.4	143060	9	AL928472	AL928472 Human DNA
40	255.2	18.4	170908	2	AC022557	AC022557 Homo sapi
41	255.2	18.4	190310	2	AC023225	AC023225 Homo sapi
42	255.2	18.4	255952	2	AL513473	AL513473 Homo sapi
43	209.8	15.1	1347	9	BC009952	BC009952 Homo sapi
44	193.2	13.9	301630	1	AE016942	AE016942 Bacteroid
45	178.6	12.9	67717	2	AC101393	AC101393 Mus muscu

ALIGNMENTS

RESULT 1
CQ868818
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CQ868818
Sequence 1 from Patent WO2004074497.
CQ868818
CQ868818.1 GI:51998752

1389 bp
DNA
Linear
PAT 13-SEP-2004

Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1
AUTHORS
TITLE
JOURNAL
Hamilton, S.R.
Endomannosidases in the modification of glycoproteins in eukaryotes
Patent: WO 2004074497-A 1 02-SEP-2004;
Hamilton, Stephen R. (US)

FEATURES

source

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/note="unnamed protein product"

CDS

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LHVFSWYGNPDGKTYHNPVLEHMDPRKAKYRGGRRPPDIDSSPYELGS
YSRDPSVETTRKQRKRSASIGTALSWTPPVVDNNGEETDNLVTLIDKAKTKK
VYHILPYSNRDQNNYKAVKYLIDRYGNHAPYRYKTKGNALPMFYATNGFTYSS
KMANLITGSGRSIRNSPYDGLFIALIVEKHKYDILQSGFDIYTPYATNGFTYSS
HONWASIKLIDCKYNLIFIPSVGPGYDTSIRPMWONTRNRNGKYEYGLAALOT
RPLISTITSFEMHEGTOIEKAVKRTSNTVYLDVRPHKPGYLIELTRKMSKYSKER
ATYALDRQLPVGS"

ORIGIN

Query Match 100.0%; Score 1389; DB 6; Length 1389;
Best Local Similarity 100.0%; Pred. No. 1.1e-298;
Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCAAGTTTGGAGAGAGACTTGACATTCATTGGCACTTTTATTCATTATTATTTTC 60